RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/537,648_

Source: _PCT_

Date Processed by STIC: _5/26/06_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 05/26/2006
PATENT APPLICATION: US/10/537,648   TIME: 07:56:25

Input Set : **A:\0380-P03063US1 seq listing.txt**
Output Set: **N:\CRF4\05262006\J537648.raw**

```
 4 <110> APPLICANT: Xiao, Zhi-Cheng
 6 <120> TITLE OF INVENTION: Peptides, Antibodies Thereto, and Their
 7       Use in the Treatment of Central Nervous System Damage
10 <130> FILE REFERENCE: 0380-P03063US1
12 <140> CURRENT APPLICATION NUMBER: US 10/537,648
13 <141> CURRENT FILING DATE: 2005-06-06
15 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/005323
16 <151> PRIOR FILING DATE: 2003-12-05
18 <150> PRIOR APPLICATION NUMBER: US 60/431,620
19 <151> PRIOR FILING DATE: 2002-12-06
21 <160> NUMBER OF SEQ ID NOS: 35
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 7
27 <212> TYPE: PRT
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
33 <400> SEQUENCE: 1
34 Tyr Leu Thr Gln Pro Gln Ser
35  1               5
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 7
40 <212> TYPE: PRT
41 <213> ORGANISM: Artificial Sequence
43 <220> FEATURE:
44 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
46 <400> SEQUENCE: 2
47 Gly Ser Leu Pro His Ser Leu
48  1               5
51 <210> SEQ ID NO: 3
52 <211> LENGTH: 7
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial Sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
59 <400> SEQUENCE: 3
60 Thr Gln Leu Phe Pro Pro Gln
61  1               5
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 7
66 <212> TYPE: PRT
67 <213> ORGANISM: Artificial Sequence
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```
69 <220> FEATURE:
70 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
72 <400> SEQUENCE: 4
73 His Ser Ile Pro Asp Asn Ile
74 1                 5
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 7
79 <212> TYPE: PRT
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
85 <400> SEQUENCE: 5
86 His His Met Pro His Asp Lys
87 1                 5
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 7
92 <212> TYPE: PRT
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
98 <400> SEQUENCE: 6
99 Tyr Thr Thr Pro Pro Ser Pro
100 1                 5
103 <210> SEQ ID NO: 7
104 <211> LENGTH: 7
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: From a phage library that displays random 7-mers
111 <400> SEQUENCE: 7
112 Gln Leu Pro Leu Met Pro Arg
113 1                 5
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 508
118 <212> TYPE: PRT
119 <213> ORGANISM: Rattus norvegicus
121 <400> SEQUENCE: 8
122 Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
123 1                 5                   10                  15
124 Ser Arg Gly Gly His Trp Gly Ala Trp Met Pro Ser Ser Ile Ser Ala
125             20                  25                  30
126 Phe Glu Gly Thr Cys Val Ser Ile Pro Cys Arg Phe Asp Phe Pro Asp
127         35                  40                  45
128 Glu Leu Arg Pro Ala Val Val His Gly Val Trp Tyr Phe Asn Ser Pro
129     50                  55                  60
130 Tyr Pro Lys Asn Tyr Pro Pro Val Val Phe Lys Ser Arg Thr Gln Val
131 65                  70                  75                  80
132 Val His Glu Ser Phe Gln Gly Arg Ser Arg Leu Leu Gly Asp Leu Gly
133             85                  90                  95
```

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```
134 Leu Arg Asn Cys Thr Leu Leu Leu Ser Thr Leu Ser Pro Glu Leu Gly
135             100                 105                 110
136 Gly Lys Tyr Tyr Phe Arg Gly Asp Leu Gly Gly Tyr Asn Gln Tyr Thr
137         115                 120                 125
138 Phe Ser Glu His Ser Val Leu Asp Ile Ile Asn Thr Pro Asn Ile Val
139     130                 135                 140
140 Val Pro Pro Glu Val Val Ala Gly Thr Glu Val Glu Val Ser Cys Met
141 145                 150                 155                 160
142 Val Pro Asp Asn Cys Pro Glu Leu Arg Pro Glu Leu Ser Trp Leu Gly
143             165                 170                 175
144 His Glu Gly Leu Gly Glu Pro Thr Val Leu Gly Arg Leu Arg Glu Asp
145             180                 185                 190
146 Glu Gly Thr Trp Val Gln Val Ser Leu Leu His Phe Val Pro Thr Arg
147         195                 200                 205
148 Glu Ala Asn Gly His Arg Leu Gly Cys Gln Ala Ala Phe Pro Asn Thr
149     210                 215                 220
150 Thr Leu Gln Phe Glu Gly Tyr Ala Ser Leu Asp Val Lys Tyr Pro Pro
151 225                 230                 235                 240
152 Val Ile Val Glu Met Asn Ser Ser Val Glu Ala Ile Glu Gly Ser His
153             245                 250                 255
154 Val Ser Leu Leu Cys Gly Ala Asp Ser Asn Pro Pro Pro Leu Leu Thr
155             260                 265                 270
156 Trp Met Arg Asp Gly Met Val Leu Arg Glu Ala Val Ala Glu Ser Leu
157         275                 280                 285
158 Tyr Leu Asp Leu Glu Glu Val Thr Pro Ala Glu Asp Gly Ile Tyr Ala
159     290                 295                 300
160 Cys Leu Ala Glu Asn Ala Tyr Gly Gln Asp Asn Arg Thr Val Glu Leu
161 305                 310                 315                 320
162 Ser Val Met Tyr Ala Pro Trp Lys Pro Thr Val Asn Gly Thr Val Val
163             325                 330                 335
164 Ala Val Glu Gly Glu Thr Val Ser Ile Leu Cys Ser Thr Gln Ser Asn
165             340                 345                 350
166 Pro Asp Pro Ile Leu Thr Ile Phe Lys Glu Lys Gln Ile Leu Ala Thr
167         355                 360                 365
168 Val Ile Tyr Glu Ser Gln Leu Gln Leu Glu Leu Pro Ala Val Thr Pro
169     370                 375                 380
170 Glu Asp Asp Gly Glu Tyr Trp Cys Val Ala Glu Asn Gln Tyr Gly Gln
171 385                 390                 395                 400
172 Arg Ala Thr Ala Phe Asn Leu Ser Val Glu Phe Ala Pro Ile Ile Leu
173             405                 410                 415
174 Leu Glu Ser His Cys Ala Ala Ala Arg Asp Thr Val Gln Cys Leu Cys
175             420                 425                 430
176 Val Val Lys Ser Asn Pro Glu Pro Ser Val Ala Phe Glu Leu Pro Ser
177         435                 440                 445
178 Arg Asn Val Thr Val Asn Glu Thr Glu Arg Glu Phe Val Tyr Ser Glu
179     450                 455                 460
180 Arg Ser Gly Leu Leu Leu Thr Ser Ile Leu Thr Leu Arg Gly Gln Ala
181 465                 470                 475                 480
182 Gln Ala Pro Pro Arg Val Ile Cys Thr Ser Arg Asn Leu Tyr Gly Thr
```

```
183                     485                 490                     495
184 Gln Ser Leu Glu Leu Pro Phe Gln Gly Ala His Arg
185             500                 505
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 205
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 9
194 Cys Pro Cys Ala Ser Ser Ala Gln Val Leu Gln Glu Leu Leu Ser Arg
195 1               5                   10                  15
196 Ile Glu Met Leu Glu Arg Glu Val Ser Val Leu Arg Asp Gln Cys Asn
197             20                  25                  30
198 Ala Asn Cys Cys Gln Glu Ser Ala Ala Thr Gly Gln Leu Asp Tyr Ile
199         35                  40                  45
200 Pro His Cys Ser Gly His Gly Asn Phe Ser Phe Glu Ser Cys Gly Cys
201     50                  55                  60
202 Ile Cys Asn Glu Gly Trp Phe Gly Lys Asn Cys Ser Glu Pro Tyr Cys
203 65                  70                  75                  80
204 Pro Leu Gly Cys Ser Ser Arg Gly Val Cys Val Asp Gly Gln Cys Ile
205                 85                  90                  95
206 Cys Asp Ser Glu Tyr Ser Gly Asp Asp Cys Ser Glu Leu Arg Cys Pro
207             100                 105                 110
208 Thr Asp Cys Ser Ser Arg Gly Leu Cys Val Asp Gly Glu Cys Val Cys
209             115                 120                 125
210 Glu Glu Pro Tyr Thr Gly Glu Asp Cys Arg Glu Leu Arg Cys Pro Gly
211         130                 135                 140
212 Asp Cys Ser Gly Lys Gly Arg Cys Ala Asn Gly Thr Cys Leu Cys Glu
213 145                 150                 155                 160
214 Glu Gly Tyr Val Gly Glu Asp Cys Gly Gln Arg Gln Cys Leu Asn Ala
215                 165                 170                 175
216 Cys Ser Gly Arg Gly Gln Cys Glu Glu Gly Leu Cys Val Cys Glu Glu
217             180                 185                 190
218 Gly Tyr Gln Gly Pro Asp Cys Ser Ala Val Ala Pro Pro
219         195                 200                 205
222 <210> SEQ ID NO: 10
223 <211> LENGTH: 185
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 10
228 Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
229 1               5                   10                  15
230 Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
231             20                  25                  30
232 Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
233         35                  40                  45
234 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
235     50                  55                  60
236 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
237 65                  70                  75                  80
```

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PATENT APPLICATION: US/10/537,648   TIME: 07:56:25

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```
238 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
239                 85              90              95
240 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
241             100             105             110
242 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
243         115             120             125
244 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
245     130             135             140
246 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
247 145             150             155             160
248 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
249             165             170             175
250 Lys Arg Arg Gly Ser Ser Gly Ser Val
251             180             185
254 <210> SEQ ID NO: 11
255 <211> LENGTH: 66
256 <212> TYPE: PRT
257 <213> ORGANISM: Homo sapiens
259 <400> SEQUENCE: 11
260 Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
261 1               5               10              15
262 His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
263             20              25              30
264 Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
265         35              40              45
266 Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
267     50              55              60
268 Leu Lys
269 65
272 <210> SEQ ID NO: 12
273 <211> LENGTH: 973
274 <212> TYPE: PRT
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Fusion protein
280 <220> FEATURE:
281 <221> NAME/KEY: VARIANT
282 <222> LOCATION: (509)...(511)
283 <223> OTHER INFORMATION: Polyalanine linker
285 <220> FEATURE:
286 <221> NAME/KEY: VARIANT
287 <222> LOCATION: (717)...(719)
288 <223> OTHER INFORMATION: Polyalanine linker
290 <220> FEATURE:
291 <221> NAME/KEY: VARIANT
292 <222> LOCATION: (905)...(907)
293 <223> OTHER INFORMATION: Polyalanine linker
295 <400> SEQUENCE: 12
296 Met Ile Phe Leu Thr Thr Leu Pro Leu Phe Trp Ile Met Ile Ser Ala
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VERIFICATION SUMMARY   DATE: 05/26/2006
PATENT APPLICATION: **US/10/537,648**   TIME: 07:56:26

Input Set : **A:\0380-P03063US1 seq listing.txt**
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